

Tetrapods - Zonation based on species, functional and food web link diversity

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This code plots biodiversity accumulation curves and priority maps for Zonation outputs

Zonation Runs:

Metawebs: 1. Adult-only interactions 'LinksAdult' 2. Interactions all life stages "LinksAll"

Biodiversity categories: 1. Species 2. Predator-prey food web links (see metawebs options)

3. Stochastic Block Model Groups - Size 'GroupsSz' 4. Stochastic Block Model Groups - Probability 'GroupsPr'

Zonation optimization 1. Core Area 'CAZ' 2. Adv. Benefit Function 'ABF'

Land Tenure 1. Optimal - all of Europe considered 2. eu - protected areas mask

Step 1: summarize information for pixel-based removal from Zon files

```
# functions page
source("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km/TetrapodFunctionion

setwd("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km/ZonationOUT")

outputs <- gsub(".rank.compressed.tif","",list.files(pattern = "rank.compressed.tif"))

## subset to only runs for ENTIRE study area = 'optimal'
outputs <- outputs[ grep("optimal",outputs) ]

codes <- outputs

Tetra.Array <- run.curves.Tetrapods(outputs,codes)

setwd("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km")
#save(Tetra.Array,file='Tetrapods.Array.Rdata')
```

Step 2: plot biod. accumulation curves - how much different biod. metrics are captured for % area protected

```
setwd("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km")
source("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km/TetrapodFunctionion

load("Tetrapods.Array.Rdata")

cArray <- Tetra.Array

c1 <- "#878787"
c2 <- "#d6604d"
c3 <- "blue"
```

```

layrs <- c(dimnames(cArray)[[3]])

metrics <- c(dimnames(cArray)[[2]])

#fig 1 -----
setwd("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km")

#pdf(file="FigCurves1.pdf",width=12,height=8)

par(mfrow=c(1,2))
par(mar=c(5,5,2,2))
cx <- 1.3

#1. species
metrics <- rep("ScaledSumPropRichness",length(layrs))
colrs <- c(rep(c1,4),rep(c2,2),rep(c3,2))
linet <- c(rep(c(1,2),length(layrs)))

plot.curve.ov(cArray,layrs,metrics,colrs,linet,xlim=c(0,0.2),ylim=c(0,1.0))
axis(2,at = c(0.1,0.2,0.3,0.4,0.5,0.6,0.70,0.80,0.90,1.0),
      labels=c(10,20,30,40,50,60,70,80,90,100),las=1, col="black", ylab="",col.lab='black',col.axis='black',
      mtext("% Spatial Range Species Protected",side=2,col='black',padj=-3,cex=cx))

axis(1,at = c(.10,.20,.30,.40,.50,.60,.70,.80,.90,1),
      labels=c(10,20,30,40,50,60,70,80,90,100),las=1, col="black", ylab="",col.lab='black',col.axis='black',
      mtext("% Land Protected",side=1,col='black',padj=2.5,cex=cx))

legend("bottomright", # position
      legend = c("Groups","Links","Species"),
      lty = c(1,1),
      title = "",
      col = c(c1,c2,c3),
      text.col = c(c1,c2,c3),
      cex = 1,
      bty = "n") # border

#2. rare species
metrics <- rep("ScaledSumPropRichnessRareSp",length(layrs))

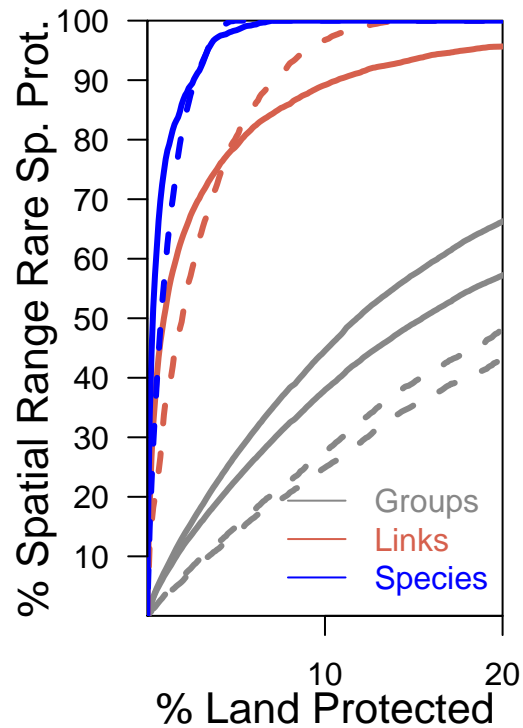
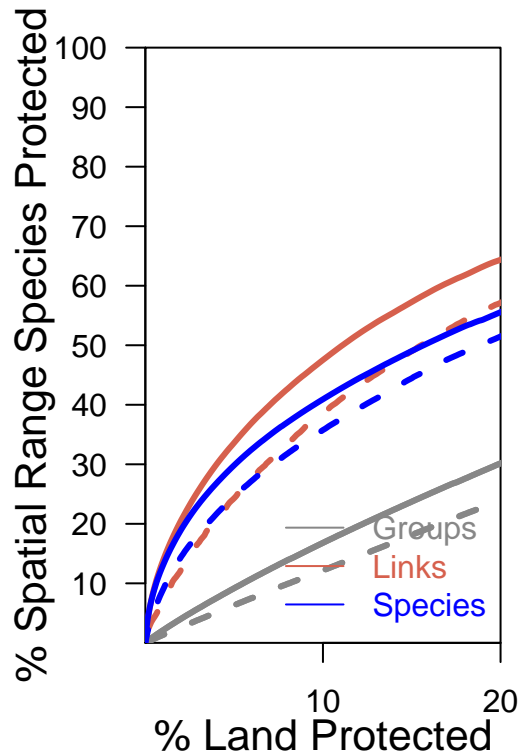
plot.curve.ov(cArray,layrs,metrics,colrs,linet,xlim=c(0,0.2),ylim=c(0,1))
axis(2,at = c(0.1,0.2,0.3,0.4,0.5,0.6,0.70,0.80,0.90,1.0),
      labels=c(10,20,30,40,50,60,70,80,90,100),las=1, col="black", ylab="",col.lab='black',col.axis='black',
      mtext("% Spatial Range Rare Sp. Prot.",side=2,col='black',padj=-3,cex=cx))

axis(1,at = c(.10,.20,.30,.40,.50,.60,.70,.80,.90,1),
      labels=c(10,20,30,40,50,60,70,80,90,100),las=1, col="black", ylab="",col.lab='black',col.axis='black',
      mtext("% Land Protected",side=1,col='black',padj=2.5,cex=cx))

legend("bottomright", # position
      legend = c("Groups","Links","Species"),

```

```
lty = c(1,1),
title = "",
col = c(c1,c2,c3),
text.col = c(c1,c2,c3),
cex = 1,
bty = "n") # border
```



```
#dev.off()
```

```
#-----
```

Step 3: plot maps

```
library(raster)
```

```
## Warning: package 'raster' was built under R version 3.5.2
```

```
## Loading required package: sp
```

```
library(RColorBrewer)
```

```
setwd("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km/ZonationOUT/")
outputs <- gsub(".rank.compressed.tif","",list.files(pattern = "rank.compressed.tif"))
```

```
# optimal maps
```

```
outputs <- outputs[grep('optimal',outputs)]
```

```

setwd("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km/ZonationOUT/")

gr.pr.abf.opt <- raster("GroupsPrABFoptimal10km.rank.compressed.tif")
gr.pr.caz.opt <- raster("GroupsPrCAZoptimal10km.rank.compressed.tif")
gr.sz.abf.opt <- raster("GroupsSzABFoptimal10km.rank.compressed.tif")
gr.sz.caz.opt <- raster("GroupsSzCAZoptimal10km.rank.compressed.tif")
li.ad.caz.opt <- raster("LinksAdultCAZoptimal10km.rank.compressed.tif")
li.ad.abf.opt <- raster("LinksAdultABFoptimal10km.rank.compressed.tif")
sp.abf.opt <- raster("SpeciesABFoptimal10km.rank.compressed.tif")
sp.caz.opt <- raster("SpeciesCAZoptimal10km.rank.compressed.tif")

#set up gradient colors

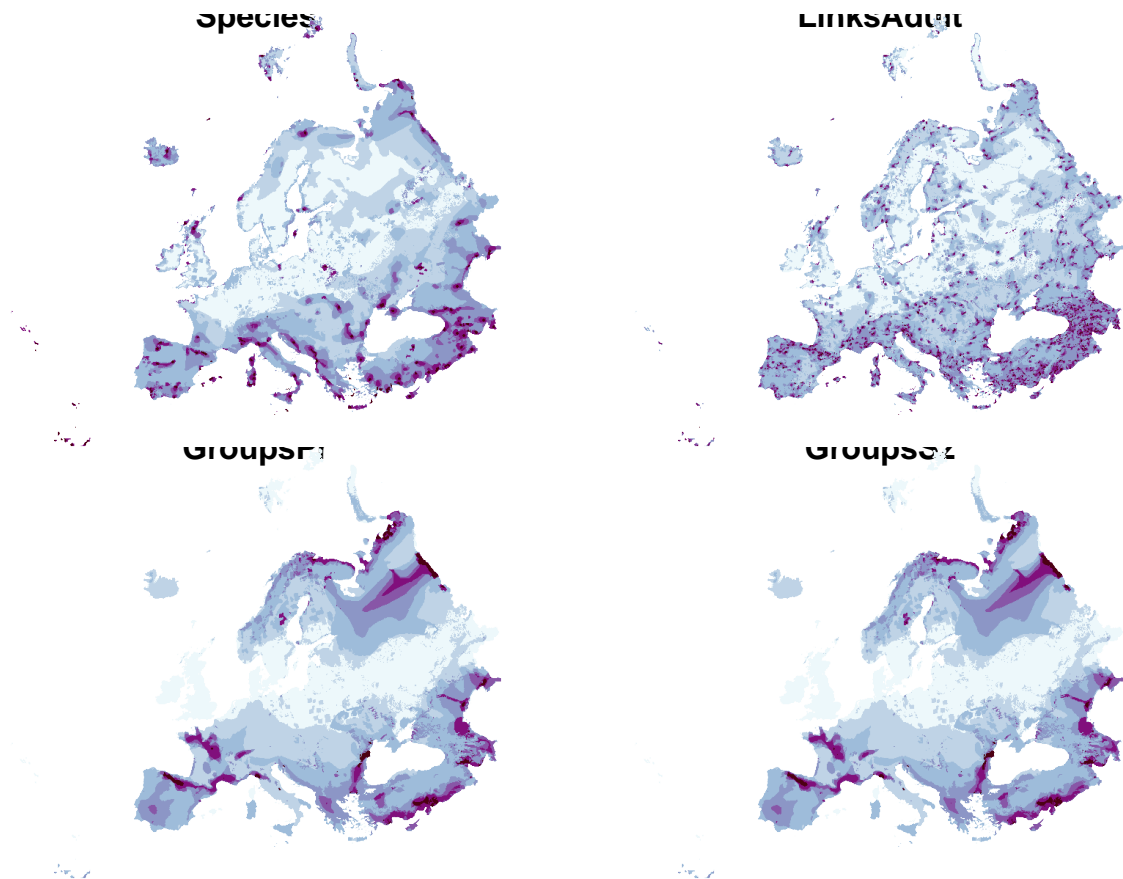
# color brewer 6-class BuPu + one
c1 <- "#edf8fb"
c2 <- "#bfd3e6"
c3 <- "#9ebcda"
c4 <- "#8c96c6"
c5 <- "#8856a7"
c6 <- "#810f7c"
c7 <- "#4c0013" #hex monochromatic
#col.protected <- "#006d2c"

breakpoints <- c(0,0.25,0.50,0.75,0.90,0.95,0.99,1.0)
colz <- c(c1,c2,c3,c4,c5,c6,c7)

setwd("~/Documents/Manuscripts/EuropeanFoodWebCons/ConservationLinksPaper/Zonation10km/")

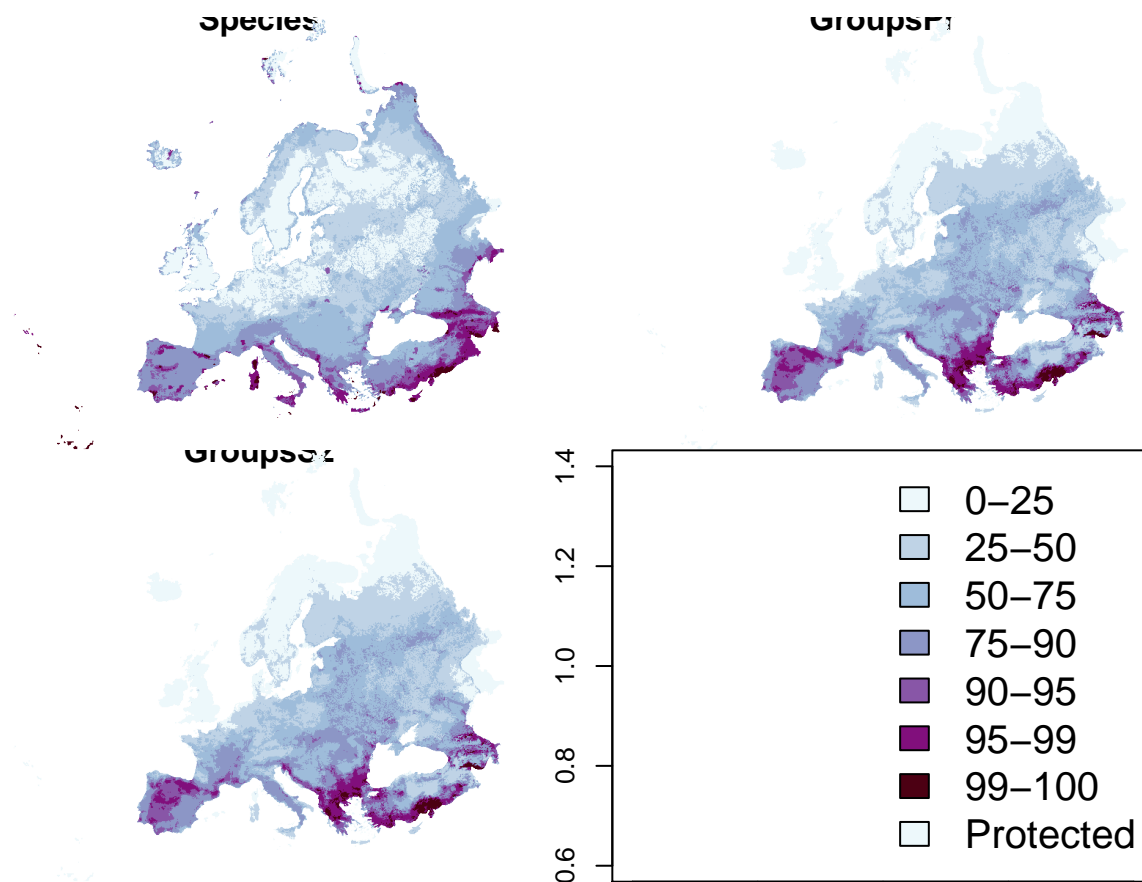
#png(filename = "TetraPriOptimalCAZ.png",width = 1200, height = 1200, units = "px")
#caz
par(mfrow=c(2,2))
par(mar=c(.01,.01,.01,.01))
plot(sp.caz.opt,breaks=breakpoints,col=colz,axes=F,legend=F,box=F,main='Species')
plot(li.ad.caz.opt,breaks=breakpoints,col=colz,axes=F,legend=F,box=F,main='LinksAdult')
plot(gr.pr.caz.opt,breaks=breakpoints,col=colz,axes=F,legend=F,box=F,main='GroupsPr')
plot(gr.sz.caz.opt,breaks=breakpoints,col=colz,axes=F,legend=F,box=F,main='GroupsSz')

```



```
#dev.off()

#png(filename = "TetraPriOptimalABF.png",width = 1200, height = 1200, units = "px")
#abf
par(mfrow=c(2,2))
par(mar=c(.01,.01,.01,.01))
plot(sp.abf.opt,breaks=breakpoints,col=colz,axes=F,legend=F,box=F,main='Species')
plot(gr.pr.abf.opt,breaks=breakpoints,col=colz,axes=F,legend=F,box=F,main='GroupsPr')
plot(gr.sz.abf.opt,breaks=breakpoints,col=colz,axes=F,legend=F,box=F,main='GroupsSz')
plot(1,1,col='white')
legend("bottomright",inset=c(0,0), # position
      legend = c("0-25", "25-50", "50-75","75-90","90-95","95-99","99-100","Protected"),
      title = "",
      fill = colz,
      cex = 1.5,
      bty = "n") # border
```



```
#ev.off()

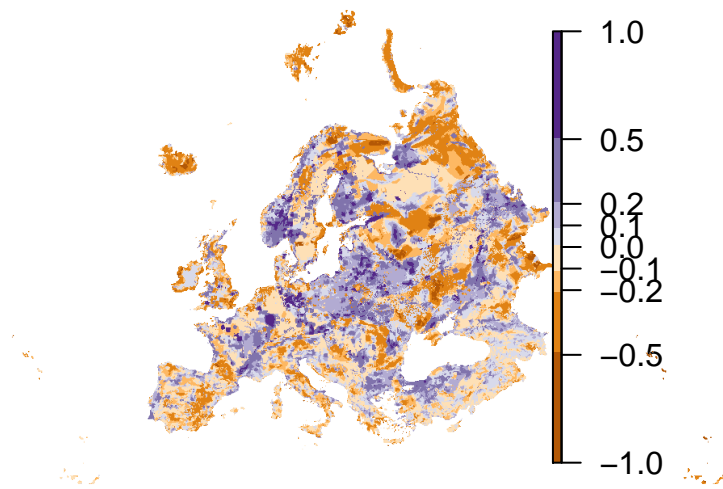
#png(filename = "DiffMaps.png",width = 1200, height = 600, units = "px")

par(mfrow=c(1,2))
diff <- li.ad.caz.opt - sp.caz.opt
colors <- c( colorRampPalette(brewer.pal(8,'PuOr'))(8))

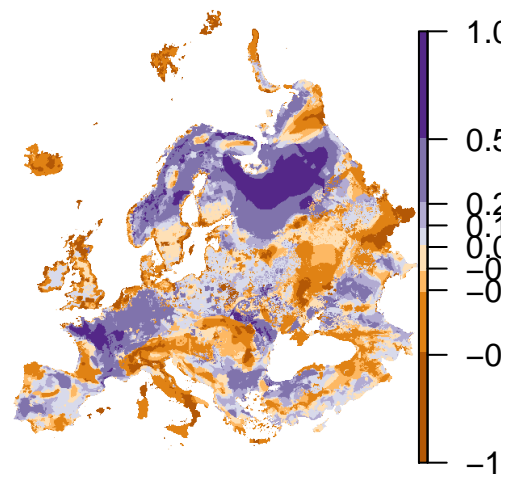
breakpoints <- c(-1,-0.5,-0.2,-0.1,0,0.1,0.2,0.5,1)
plot(diff,breaks=breakpoints,col=colors,axes=F,box=F,legend=T,main="Links minus species")

diff <- gr.pr.caz.opt - sp.caz.opt
plot(diff,breaks=breakpoints,col=colors,axes=F,box=F,legend=T,main="Groups minus species")
```

Links minus species



Groups minus species



`#dev.off()`